Genetic diversity and phylogeography of cassava mosaic geminiviruses in Madagascar

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Cassava mosaic disease (CMD) caused by cassava mosaic geminiviruses (CMGs, *Geminiviridae*) is a major threat on cassava production throughout Africa. In Madagascar, severe symptoms with high prevalence of CMD were observed. From 700 mostly symptomatic cassava leaves, we undertook molecular characterization of the CMGs involved. The PCR diagnosis confirmed the presence of CMGs in Madagascar and six species were detected with the frequent occurrence of mixed infections. Based on rolling circle amplification, cloning and sequencing, we obtained full genome sequences of 281 DNA-A and 119 DNA-B of CMGs. DNA-A sequences were most closely related to those of *African cassava mosaic virus* (ACMV), *South African cassava mosaic virus* (SACMV), *East African cassava mosaic virus* (EACMV), *East African cassava mosaic Cameroon virus* (EACMCV), *East African cassava mosaic Kenya virus* (EACMKV) and a new species named Cassava mosaic Madagascar virus (CMMGV). DNA-B sequences were most closely related to those of ACMV, EACMKV, EACMCV and CMMGV. Phylogenetic reconstruction allowed to assess the geographical structure of CMG populations and to determine the recent history of CMG migrations in Madagascar. Taken together, our results point to Madagascar as a potential major center of begomovirus diversity.